

ABSTRACT OF THE DISCLOSURE

This invention relates to methods and systems for *in silico* or bioinformatic modeling of cellular metabolism. The invention includes methods and systems for modeling cellular metabolism of an organism, comprising constructing a flux balance analysis model, and applying constraints to the flux balance analysis model, the constraints selected from the set consisting of: qualitative kinetic information constraints, qualitative regulatory information constraints, and differential DNA microarray experimental data constraints. In addition, the present invention provides for computational procedures for solving metabolic problems.